

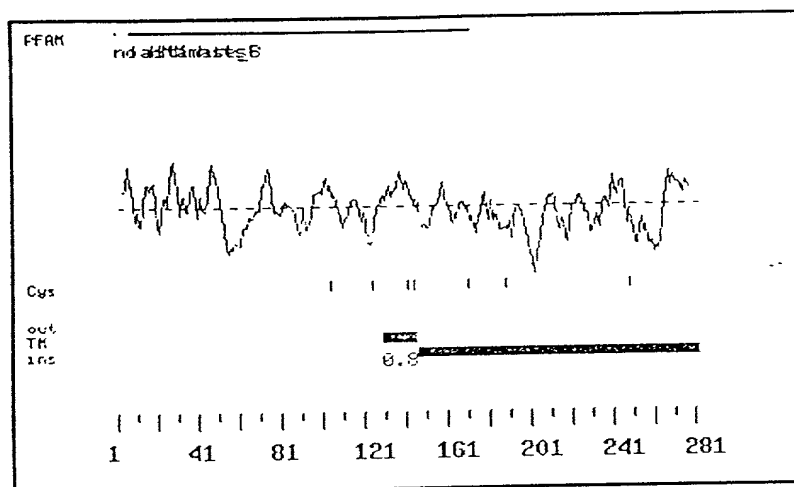
Input file Fbh50566FL.seq; Output File 50566.trans
Sequence length 1154

	M	K	V	K	V	I	P	V	L	E	D	N	Y	M	14					
CGGACGCGTGGGTCCGTGACC	ATG	AAG	GTC	AAG	GTC	ATC	CCC	GTG	CTC	GAG	GAC	AAC	TAC	ATG	42					
Y	L	V	I	E	E	L	T	R	E	A	V	A	V	D	V	A	V	P	K	34
TAC	CTG	GTC	ATC	GAG	GAG	CTC	ACG	CGC	GAG	GCG	GTG	GCC	GTG	GAC	GTG	GCT	GTG	CCC	AAG	102
R	L	L	E	I	V	G	R	E	G	V	S	L	T	A	V	L	T	T	H	54
AGG	CTG	CTG	GAG	ATC	GTG	GGC	CGG	GAG	GGG	GTG	TCT	CTG	ACC	GCT	GTG	CTG	ACC	ACC	CAC	162
H	H	W	D	H	A	R	G	N	P	E	L	A	R	L	R	P	G	L	A	74
CAT	CAC	TGG	GAC	CAC	GCG	CGG	GGA	AAC	CCG	GAG	CTG	GCG	CGG	CTT	CGT	CCC	GGG	CTG	GCG	222
V	L	G	A	D	E	R	I	F	S	L	T	R	R	L	A	H	G	E	E	94
GTG	CTG	GGC	GCG	GAC	GAG	CGC	ATC	TTC	TCG	CTG	ACG	CGC	AGG	CTG	GCG	CAC	GGC	GAG	GAG	282
L	R	F	G	A	I	H	V	R	C	L	L	T	P	G	H	T	A	G	H	114
CTG	CGG	TTC	GGG	GCC	ATC	CAC	GTG	CGT	TGC	CTC	CTG	ACG	CCC	GGC	CAC	ACC	GCC	GGC	CAC	342
M	S	Y	F	L	W	E	D	D	C	P	D	P	P	A	L	F	S	G	D	134
ATG	AGC	TAC	TTC	CTG	TGG	GAG	GAC	GAT	TGC	CCG	GAC	CCA	CCC	GCC	CTG	TTC	TCG	GGC	GAC	402
A	L	S	V	A	G	C	G	S	C	L	E	G	S	A	Q	Q	M	Y	Q	154
GCG	CTG	TCG	GTG	GCC	GGC	TGC	GGC	TCG	TGC	CTG	GAG	GGC	AGC	GCC	CAG	CAG	ATG	TAC	CAG	462
S	L	A	E	L	G	T	L	P	P	E	T	K	V	F	C	G	H	E	H	174
AGC	CTG	GCC	GAG	CTG	GGT	ACC	CTG	CCC	CCC	GAG	ACG	AAG	GTG	TTC	TGC	GGC	CAC	GAG	CAC	522
T	L	S	N	L	E	F	A	Q	K	V	E	P	C	N	D	H	V	R	A	194
ACG	CTT	AGC	AAC	CTG	GAG	TTT	GCC	CAG	AAA	GTG	GAG	CCC	TGC	AAC	GAC	CAC	GTG	AGA	GCC	582
K	L	S	W	A	K	K	R	D	E	D	D	V	P	T	V	P	S	T	L	214
AAG	CTG	TCC	TGG	GCT	AAG	AAG	AGG	GAT	GAG	GAT	GAC	GTG	CCC	ACT	GTG	CCG	TCG	ACT	CTG	642
G	E	E	R	L	Y	N	P	F	L	R	V	A	E	E	P	V	R	K	F	234
GGC	GAG	GAG	CGC	CTC	TAC	AAC	CCC	TTC	CTG	CGG	GTG	GCA	GAG	GAG	CCG	GTG	CGC	AAG	TTC	702
T	G	K	A	V	P	A	D	V	L	E	A	L	C	K	E	R	A	R	F	254
ACG	GGC	AAG	GCG	GTC	CCC	GCC	GAC	GTC	CTG	GAG	GCG	CTA	TGC	AAG	GAG	CGG	GCG	CGC	TTC	762
E	Q	A	G	E	P	R	Q	P	Q	A	R	A	L	L	A	L	Q	W	G	274
GAA	CAG	GCG	GGC	GAG	CCG	CGG	CAG	CCA	CAG	GCG	CGG	GCC	CTC	CTT	GCG	CTG	CAG	TGG	GGG	822
L	L	S	A	A	P	H	D	*												283
CTC	CTG	AGT	GCA	GCC	CCA	CAC	GAC	TGA												849

GCCACCCAGACCCTCACAGGGCTGGGGCCTGCGTCCCTCCTCGTGACCTCGGCCAGCTGGACCCACATGAGGGCCACCT
CTGGAACCTTCTTCGAGGCCCTGGCCAGCCATCTGCCCAGCCTCGGAGGGTGGGCAACCTGGTGCTTCCCGGGTGGACA
CACAGGACCACTCAGTGGGGCCTGTGTGGGCGCCGAGACCTGGGTGTCTGGGAAGTGGGGCACACGGGGCCTCCGAACCT
ATGAATAAAGCTTTGAAAGCCGTTGTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 1

Analysis of 50566 (282 aa)



>50566

MKVKVIPVLEDNYMYLVIEELTREAVAVDVAVPKRLLIIVGREGVSLTAVLTTHHHWDHA
RGNPELARLRPGLAVLGADERIFSLTRRLAHGEELRFGAIHVRCLLTPGHTAGHMSYFLW
EDDCPDPPALFSGDALSVAGCGSCLEGSAAQMYQSLAELGTLPPETKVFCGHEHTLSNLE
FAQKVEPCNDHVRAKLSWAKKRDEDDVPTVPSTLGEERLYNPFRLRVAEEPVRKFTGKAVP
ADVLEALCKERARFEQAGEPRQPQARALLALQWGLLSAAPHD

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
129	145	out-->ins	0.8

FIGURE 2

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
lactamase_B	Metallo-beta-lactamase superfamily	133.3	4.4e-36	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
lactamase_B	1/1	7	172	..	1 218 {}	133.3	4.4e-36

Alignments of top-scoring domains:

lactamase_B: domain 1 of 1, from 7 to 172: score 133.3, E = 4.4e-36

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*->pglvdsnaylvedddggPgeaaliDpGttapaaeallrllkdggple
p l d+++ylv+ + + +ea+ +D + + +++++ ++
50566 7 PVLEDNYMYLVIEELT--REAVAVDVAVPKR-LLEIVGREG----- 44

nikkidaiilTHaHaDHiGGapaellekfgvpvaahaaevyaskdylgyg
+++ TH+H+DH+ G+p el+++ + + v +++
50566 45 --VSLTAVLTTHHHWDHARGNP-ELARLRP-----GLAV-----LGA 78

edrlk..dealkdgdltflivieelrvglgvelevihtPGtHTpgsivvy
++r+ + ++ l++g+ elr+g ++++++ tPG HT g+++y+
50566 79 DERIFslTRRLAHGE-----ELRFG-AIHVRCLLTPG-HTAGHMSYF 118

lpeekggespkivvLftGDtlfsggcpdgetdplgrtdllggdpaellie
l+e+ +p +Lf+GD+l +gc g l+g++ +++
50566 119 LWEDDCPDPP---ALFSGDALSVAGC-----GS---CLEGSAQMYQ 154

sleqsesllkl1lpddtvvypGH<-*
sl +l +lp++t v++GH
50566 155 SLA---ELG-TLPPETKVFCGH 172

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FIGURE 3

